IFW16

RAW SEQUENCE LISTING   DATE: 07/26/2006
PATENT APPLICATION: **US/10/632,780A**   TIME: 09:34:00

Input Set : **N:\Crf4\07252006\J632780.raw**
Output Set: **N:\CRF4\07252006\J632780A.raw**

SEQUENCE LISTING

```
 1 (1) GENERAL INFORMATION:
 2      (i) APPLICANT: Philipp, Mario T.
 3     (ii) TITLE OF INVENTION: Surface Antigens and Proteins Useful in
 4                              Compositions for the Diagnosis and Prevention of Lyme
 5                              Disease
 6    (iii) NUMBER OF SEQUENCES: 14
 7     (iv) CORRESPONDENCE ADDRESS:
 8          (A) ADDRESSEE: Howson and Howson
 9          (B) STREET: 501 Office Center Drive, Suite 210
10          (C) CITY: Fort Washington
11          (D) STATE: Pennsylvania
12          (E) COUNTRY: USA
13          (F) ZIP: 19034
14      (v) COMPUTER READABLE FORM:
15          (A) MEDIUM TYPE: Floppy disk
16          (B) COMPUTER: IBM PC compatible
17          (C) OPERATING SYSTEM: PC-DOS/MS-DOS
18          (D) SOFTWARE: PatentIn Release #1.0, Version #1.30
19     (vi) CURRENT APPLICATION DATA:
C--> 20          (A) APPLICATION NUMBER: US/10/632,780A
C--> 21          (B) FILING DATE: 01-Aug-2003
22          (C) CLASSIFICATION:
23    (vii) PRIOR APPLICATION DATA:
W--> 24          (A) APPLICATION NUMBER: US 09/445,803
25          (B) FILING DATE: 13-DEC-1999
W--> 26          (A) APPLICATION NUMBER: PCT/US98/13551
27          (B) FILING DATE: 29-JUN-1998
W--> 28          (A) APPLICATION NUMBER: US 60/051,271
29          (B) FILING DATE: 30-JUN-1997
30   (viii) ATTORNEY/AGENT INFORMATION:
31          (A) NAME: Bak, Mary E.
32          (B) REGISTRATION NUMBER: 31,215
33          (C) REFERENCE/DOCKET NUMBER: TUL2BUSA
34     (ix) TELECOMMUNICATION INFORMATION:
35          (A) TELEPHONE: 215-540-9200
36          (B) TELEFAX: 215-540-5818
37 (2) INFORMATION FOR SEQ ID NO: 1:
38      (i) SEQUENCE CHARACTERISTICS:
39          (A) LENGTH: 1047 base pairs
40          (B) TYPE: nucleic acid
41          (C) STRANDEDNESS: double
42          (D) TOPOLOGY: unknown
```

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```
43      (ii) MOLECULE TYPE: cDNA
44      (ix) FEATURE:
45           (A) NAME/KEY: CDS
46           (B) LOCATION: 1..1047
47      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:
48      AAG AAT AAT GAT CAT GAT AAT CAT AAG GGG ACT GTT AAG AAT GCT GTT        48
49      Lys Asn Asn Asp His Asp Asn His Lys Gly Thr Val Lys Asn Ala Val
50      1               5                   10                  15
51      GAT ATG GCA AAG GCC GCT GAG GAA GCT GCA AGT GCT GCA AGT GCT GCT        96
52      Asp Met Ala Lys Ala Ala Glu Glu Ala Ala Ser Ala Ala Ser Ala Ala
53                      20                  25                  30
54      ACT GGT AAT GCA GCG ATT GGG GAT GTT GTT AAG AAT AGT GGG GCA GCA       144
55      Thr Gly Asn Ala Ala Ile Gly Asp Val Val Lys Asn Ser Gly Ala Ala
56                      35                  40                  45
57      GCA AAA GGT GGT GAG GCG GCG AGT GTT AAT GGG ATT GCT AAG GGG ATA       192
58      Ala Lys Gly Gly Glu Ala Ala Ser Val Asn Gly Ile Ala Lys Gly Ile
59           50                  55                  60
60      AAG GGG ATT GTT GAT GCT GCT GGA AAG GCT GAT GCG AAG GAA GGG AAG       240
61      Lys Gly Ile Val Asp Ala Ala Gly Lys Ala Asp Ala Lys Glu Gly Lys
62      65                  70                  75                  80
63      TTG GAT GCT ACT GGT GCT GAG GGT ACG ACT AAC GTG AAT GCT GGG AAG       288
64      Leu Asp Ala Thr Gly Ala Glu Gly Thr Thr Asn Val Asn Ala Gly Lys
65                      85                  90                  95
66      TTG TTT GTG AAG AGG GCG GCT GAT GAT GGT GGT GAT GCA GAT GAT GCT       336
67      Leu Phe Val Lys Arg Ala Ala Asp Asp Gly Gly Asp Ala Asp Asp Ala
68                      100                 105                 110
69      GGG AAG GCT GCT GCT GCG GTT GCT GCA AGT GCT GCT ACT GGT AAT GCA       384
70      Gly Lys Ala Ala Ala Ala Val Ala Ala Ser Ala Ala Thr Gly Asn Ala
71                      115                 120                 125
72      GCG ATT GGA GAT GTT GTT AAT GGT GAT GTG GCA AAA GCA AAA GGT GGT       432
73      Ala Ile Gly Asp Val Val Asn Gly Asp Val Ala Lys Ala Lys Gly Gly
74           130                 135                 140
75      GAT GCG GCG AGT GTT AAT GGG ATT GCT AAG GGT ATA AAG GGG ATT GTT       480
76      Asp Ala Ala Ser Val Asn Gly Ile Ala Lys Gly Ile Lys Gly Ile Val
77      145                 150                 155                 160
78      GAT GCT GCT GAG AAG GCT GAT GCG AAG GAA GGG AAG TTG AAT GCT GCT       528
79      Asp Ala Ala Glu Lys Ala Asp Ala Lys Glu Gly Lys Leu Asn Ala Ala
80                      165                 170                 175
81      GGT GCT GAG GGT ACG ACT AAC GCG GAT GCT GGG AAG TTG TTT GTG AAG       576
82      Gly Ala Glu Gly Thr Thr Asn Ala Asp Ala Gly Lys Leu Phe Val Lys
83                      180                 185                 190
84      AAT GCT GGT AAT GTG GGT GGT GAA GCA GGT GAT GCT GGG AAG GCT GCT       624
85      Asn Ala Gly Asn Val Gly Gly Glu Ala Gly Asp Ala Gly Lys Ala Ala
86                      195                 200                 205
87      GCT GCG GTT GCT GCT GTT AGT GGG GAG CAG ATA TTA AAA GCG ATT GTT       672
88      Ala Ala Val Ala Ala Val Ser Gly Glu Gln Ile Leu Lys Ala Ile Val
89           210                 215                 220
90      CAT GCT GCT AAG GAT GGT GGT GAG AAG CAG GGT AAG AAG GCT GCG GAT       720
91      His Ala Ala Lys Asp Gly Gly Glu Lys Gln Gly Lys Lys Ala Ala Asp
```

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```
92       225                 230                 235                 240
93     CGT ACA AAT CCC ATT GAC GCG GCT ATT GGG GGT GCG GGT GAT AAT GAT      768
94     Arg Thr Asn Pro Ile Asp Ala Ala Ile Gly Gly Ala Gly Asp Asn Asp
95                       245                 250                 255
96     GCT GCT GCG GCG TTT GCT ACT ATG AAG AAG GAT GAT CAG ATT GCT GCT      816
97     Ala Ala Ala Ala Phe Ala Thr Met Lys Lys Asp Asp Gln Ile Ala Ala
98                       260                 265                 270
99     GCT ATG GTT CTG AGG GGA ATG GCT AAG GAT GGG CAA TTT GCT TTG AAG      864
100     Ala Met Val Leu Arg Gly Met Ala Lys Asp Gly Gln Phe Ala Leu Lys
101                   275                 280                 285
102     GAT GCT GCT GCT GCT CAT GAA GGG ACT GTT AAG AAT GCT GTT GAT ATA      912
103     Asp Ala Ala Ala Ala His Glu Gly Thr Val Lys Asn Ala Val Asp Ile
104           290                 295                 300
105     ATA AAG GCT GCT GCG GAA GCT GCA AGT GCT GCA AGT GCT GCT ACT GGT      960
106     Ile Lys Ala Ala Ala Glu Ala Ala Ser Ala Ala Ser Ala Ala Thr Gly
107     305                 310                 315                 320
108     AGT GCA GCA ATT GGG GAT GTT GTT AAT GGT AAT GGA GCA ACA GCA AAA     1008
109     Ser Ala Ala Ile Gly Asp Val Val Asn Gly Asn Gly Ala Thr Ala Lys
110                   325                 330                 335
111     GGT GGT GAT GCG AAG AGT GTT AAT GGC ATT GCT AAG GGA             1047
112     Gly Gly Asp Ala Lys Ser Val Asn Gly Ile Ala Lys Gly
113                   340                 345
115 (2) INFORMATION FOR SEQ ID NO: 2:
116     (i) SEQUENCE CHARACTERISTICS:
117         (A) LENGTH: 349 amino acids
118         (B) TYPE: amino acid
119         (D) TOPOLOGY: linear
120     (ii) MOLECULE TYPE: protein
121     (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:
122     Lys Asn Asn Asp His Asp Asn His Lys Gly Thr Val Lys Asn Ala Val
123      1                   5                  10                  15
124     Asp Met Ala Lys Ala Ala Glu Glu Ala Ala Ser Ala Ala Ser Ala Ala
125                   20                  25                  30
126     Thr Gly Asn Ala Ala Ile Gly Asp Val Val Lys Asn Ser Gly Ala Ala
127               35                  40                  45
128     Ala Lys Gly Gly Glu Ala Ala Ser Val Asn Gly Ile Ala Lys Gly Ile
129           50                  55                  60
130     Lys Gly Ile Val Asp Ala Ala Gly Lys Ala Asp Ala Lys Glu Gly Lys
131      65                  70                  75                  80
132     Leu Asp Ala Thr Gly Ala Glu Gly Thr Thr Asn Val Asn Ala Gly Lys
133                   85                  90                  95
134     Leu Phe Val Lys Arg Ala Ala Asp Asp Gly Gly Asp Ala Asp Asp Ala
135               100                 105                 110
136     Gly Lys Ala Ala Ala Ala Val Ala Ala Ser Ala Ala Thr Gly Asn Ala
137           115                 120                 125
138     Ala Ile Gly Asp Val Val Asn Gly Asp Val Ala Lys Ala Lys Gly Gly
139           130                 135                 140
140     Asp Ala Ala Ser Val Asn Gly Ile Ala Lys Gly Ile Lys Gly Ile Val
141     145                 150                 155                 160
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```
142    Asp Ala Ala Glu Lys Ala Asp Ala Lys Glu Gly Lys Leu Asn Ala Ala
143                    165             170         175
144    Gly Ala Glu Gly Thr Thr Asn Ala Asp Ala Gly Lys Leu Phe Val Lys
145                180             185             190
146    Asn Ala Gly Asn Val Gly Gly Glu Ala Gly Asp Ala Gly Lys Ala Ala
147            195             200             205
148    Ala Ala Val Ala Ala Val Ser Gly Glu Gln Ile Leu Lys Ala Ile Val
149        210             215             220
150    His Ala Ala Lys Asp Gly Gly Glu Lys Gln Gly Lys Lys Ala Ala Asp
151    225             230             235             240
152    Arg Thr Asn Pro Ile Asp Ala Ala Ile Gly Gly Ala Gly Asp Asn Asp
153                245             250             255
154    Ala Ala Ala Ala Phe Ala Thr Met Lys Lys Asp Asp Gln Ile Ala Ala
155                260             265             270
156    Ala Met Val Leu Arg Gly Met Ala Lys Asp Gly Gln Phe Ala Leu Lys
157        275             280             285
158    Asp Ala Ala Ala Ala His Glu Gly Thr Val Lys Asn Ala Val Asp Ile
159        290             295             300
160    Ile Lys Ala Ala Ala Glu Ala Ala Ser Ala Ala Ser Ala Ala Thr Gly
161    305             310             315             320
162    Ser Ala Ala Ile Gly Asp Val Val Asn Gly Asn Gly Ala Thr Ala Lys
163                325             330             335
164    Gly Gly Asp Ala Lys Ser Val Asn Gly Ile Ala Lys Gly
165                340             345
167 (2) INFORMATION FOR SEQ ID NO: 3:
168     (i) SEQUENCE CHARACTERISTICS:
169         (A) LENGTH: 283 base pairs
170         (B) TYPE: nucleic acid
171         (C) STRANDEDNESS: double
172         (D) TOPOLOGY: unknown
173     (ii) MOLECULE TYPE: DNA (genomic)
174     (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:
175     GCCGCTGGAT GGTGGTGAGA AGCAGGGTAA GAAGGCTGCG GATCGTACAA ATCCCATTGA     60
176     CGCGGCTATT GGGGGTGCGG GTGATAATGA TGCTGCTGCG GCGTTTGCTA CTATGAAGAA    120
177     GGATGATCAG ATTGCTGCTG CTATGGTTCT GAGGGGAATG GCTAAGGATG GGCAATTTGC    180
178     TTTGAAGGAT GCTGCTGCTG CTCATGAAGG GACTGTTAAG AATGCTGTTG ATATAATAAA    240
179     GGCTGCTGCG GAAGCTGCAA GTGCTGCAAG TGCTGCTACT GGT                      283
181 (2) INFORMATION FOR SEQ ID NO: 4:
182     (i) SEQUENCE CHARACTERISTICS:
183         (A) LENGTH: 233 base pairs
184         (B) TYPE: nucleic acid
185         (C) STRANDEDNESS: double
186         (D) TOPOLOGY: unknown
187     (ii) MOLECULE TYPE: DNA (genomic)
188     (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:
189     TTTATTATAT CAACAGATTC TTAACAGTCC CTTCATGAGC AGCAGCAGCA TCCTTCAAAG     60
190     CAAATTGCCC ATCCTTAGCC ATTCCCCTCA GAACCATAGC AGCAGCAATC TGATCATCCT    120
191     TCTTCATAGT AGCAAACGCC GCAGCAGCAT CATTATCACC CGCACCCCCA ATAGCCGCGT    180
192     CAATCGGATT TGTACGATCC GCAGCCTTCT TACCCTGCTT CTCACCACCA TCC           233
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```
194 (2) INFORMATION FOR SEQ ID NO: 5:
195     (i) SEQUENCE CHARACTERISTICS:
196         (A) LENGTH: 194 base pairs
197         (B) TYPE: nucleic acid
198         (C) STRANDEDNESS: double
199         (D) TOPOLOGY: unknown
200     (ii) MOLECULE TYPE: DNA (genomic)
201     (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5:
202     CCGTGCAAGC TGGGTTGAAG AAGGTTGGGG ATGTTGTTAA GAATAGTGAG GCAAAAGATG          60
203     GTGATGCGGC GAGTGTTAAT GGGATTGCTA AGGGGATAAA GGGGATTGTT GATGCTGCTG         120
204     AGAAGGCTGA TGCGAAGGAA GGGAAGTTGG TATGTGGCTG GTGCTGCTGG TGAAACTAAC         180
205     AAGGAAGCGG CCGC                                                          194
207 (2) INFORMATION FOR SEQ ID NO: 6:
208     (i) SEQUENCE CHARACTERISTICS:
209         (A) LENGTH: 369 base pairs
210         (B) TYPE: nucleic acid
211         (C) STRANDEDNESS: double
212         (D) TOPOLOGY: unknown
213     (ii) MOLECULE TYPE: DNA (genomic)
214     (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 6:
215     GCGGCCGCTT GAGGAAGCTG CAAGTGCTGC AAGTGCTGCT ACTGGTAATG CAGCGATTGG          60
216     GGATGTTGTT AAGAATAGTG GGGCAGCAGC AAAAGGTGGT GAGGCGGCGA GTGTTAATGG         120
217     GATTGCTAAG GGGATAAAGG GGATTGTTGA TGCTGCTGGA AAGGCTGATG CGAAGGAAGG         180
218     GAAGTTGGAT GCTACTGGTG CTGAGGGTAC GACTAACGTG AATGCTGGGA AGTTGTTTGT         240
219     GAAGAGGGCG GCTGATGATG GTGGTGATGC AGATGATGCT GGGAAGGCTG CTGCTGCGGT         300
220     TGCTGCAAGT GCTGCTACTG GTAATGCAGC GATTGGAGAT GTTGTTAATG GTGATGTGGC         360
221     AAAACAAAA                                                               369
223 (2) INFORMATION FOR SEQ ID NO: 7:
224     (i) SEQUENCE CHARACTERISTICS:
225         (A) LENGTH: 142 base pairs
226         (B) TYPE: nucleic acid
227         (C) STRANDEDNESS: double
228         (D) TOPOLOGY: unknown
229     (ii) MOLECULE TYPE: DNA (genomic)
230     (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 7:
231     AAGGATGGTG ATGATAAGCA GGGTAAGAAG GCTGAGGATG CTACAAATCC GATTGACGCG          60
232     GCTATTGGGG GTGCAGGTGC GGGTGCTAAT GCTGCTGCGG CGTTTAATAA TATGAAGAAG         120
233     GATGATCAGA TTGAGCGGCC GC                                                 142
235 (2) INFORMATION FOR SEQ ID NO: 8:
236     (i) SEQUENCE CHARACTERISTICS:
237         (A) LENGTH: 210 base pairs
238         (B) TYPE: nucleic acid
239         (C) STRANDEDNESS: double
240         (D) TOPOLOGY: unknown
241     (ii) MOLECULE TYPE: DNA (genomic)
242     (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 8:
243     GGTGAAACTA ACAAGGATGC TGGGAAGTTG TTTGTGAAGA AGAATGGTGA TGATGGTGGT          60
244     GATGCAGGTG ATGCTGGGAA GGCTGCTGCT GCGGTTGCTG CTGTTAGTGG GGAGCAGATA         120
245     TTAAAAGCGA TTGTTGATGC TGCTAAAGAT GGTGATAAGA CGGGGGTTAC TGATGTAAAG         180
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RAW SEQUENCE LISTING ERROR SUMMARY   DATE: 07/26/2006
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<u>**Invalid Line Length:**</u>
The rules require that a line not exceed 72 characters in length. This includes spaces.

Seq#:1; Line(s) 4

VERIFICATION SUMMARY   DATE: 07/26/2006
PATENT APPLICATION: **US/10/632,780A**   TIME: 09:34:01

Input Set : **N:\Crf4\07252006\J632780.raw**
Output Set: **N:\CRF4\07252006\J632780A.raw**

L:20 M:220 C: Keyword misspelled or invalid format, [(A) APPLICATION NUMBER:]
L:21 M:220 C: Keyword misspelled or invalid format, [(B) FILING DATE:]
L:26 M:238 W: Alpha Fields not Ordered, Reordered [(A) APPLICATION NUMBER:] of (1)(vii)
L:28 M:238 W: Alpha Fields not Ordered, Reordered [(A) APPLICATION NUMBER:] of (1)(vii)